

AP20 Rec'd PCT/PTO 20 JUL 2006

## SEQUENCE LISTING

<110> AKZO Nobel N.V.

<120> *Lawsonia intracellularis* subunit vaccines.

<130> 2004.001

<160> 18

<170> PatentIn version 3.2

<210> 1

<211> 2088

<212> DNA

<213> *Lawsonia intracellularis*

<220>

<221> CDS

<222> (16)..(2085)

<400> 1

cggaggttga ttact atg agt ctt aca gca gga atg tgg aca ggt gtt tca	51
Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser	
1 5 10	
gga ctt tta agt cat ggc gaa aag atg aat gtt att ggt aat aac ata	99
Gly Leu Leu Ser His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile	
15 20 25	
gct aac gta aat aca gta ggc ttt aaa ggc caa cgt atg gat ttc gca	147
Ala Asn Val Asn Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala	
30 35 40	
gac ttt att tat caa gat ggc ttt agt act gca ggg att aca caa att	195
Asp Phe Ile Tyr Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile	
45 50 55 60	
gga cgt ggt gta ggc att gga gct gtc atg ggg aac ttt ggt cag ggt	243
Gly Arg Gly Val Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly	
65 70 75	
agt ttt gaa acc aca act gaa gca aca gac ctt gct att ggt ggt cgt	291
Ser Phe Glu Thr Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg	
80 85 90	
gga ttt ttc aaa gtt aaa cca caa gga tca gag act tca tat tat acc	339
Gly Phe Phe Lys Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr	
95 100 105	
cgt gca ggt aat ttt cgt ttt aat aat gat gga tac tta gtt gat cct	387
Arg Ala Gly Asn Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro	
110 115 120	
cat gga tat gct ctt cag ggt tgg aaa att gat aat act gaa ggg cca	435
His Gly Tyr Ala Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro	
125 130 135 140	
caa cgt atc tca ggt ggt gtt aat cca ggt aca aat act tgc cag att	483

Gln Arg Ile Ser Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile	
145 150 155	
atg ggt aca ggt gaa cca aca gat atc cgt ctt gat act tgg aca gtt	531
Met Gly Thr Gly Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val	
160 165 170	
gca cct tta cag aca aca aat gta agt ttt aac gta aac ctt tct tct	579
Ala Pro Leu Gln Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser	
175 180 185	
gat aaa tct gga gat aaa tct caa aac gtt aat agt cca ttt acc tca	627
Asp Lys Ser Gly Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser	
190 195 200	
tta ttt aat ata tgg aat ggt aaa caa cca agt gaa cct aac aat cca	675
Leu Phe Asn Ile Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro	
205 210 215 220	
cct atg cct gaa agt gca tat agt tat cag aca tct att aag gta tat	723
Pro Met Pro Glu Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr	
225 230 235	
gat gaa gct ggt gga aca cat aca tta aca gtc tat ttt gac caa gtt	771
Asp Glu Ala Gly Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val	
240 245 250	
tct cct aaa gac tac aaa ggt ggt gga agt gga gaa agt gta tgg gaa	819
Ser Pro Lys Asp Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu	
255 260 265	
tac gtt gtt act atg gat cct tct gaa gat aat cgc caa gtt tct gtt	867
Tyr Val Val Thr Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val	
270 275 280	
ggt ggt aac att gtg gac atc aaa gat act aaa gct gca gga atg tta	915
Gly Gly Asn Ile Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu	
285 290 295 300	
atg tca gga aca ttg agt ttt gat agc tca gga aaa ctt gca aac caa	963
Met Ser Gly Thr Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln	
305 310 315	
agt gca tat tgg ctg aat ggt tca cgt aag cct gca gtt gat cct gca	1011
Ser Ala Tyr Ser Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala	
320 325 330	
acc gga gct ctt att aat ggt aat ggt ttt act att gat aga gat gga	1059
Thr Gly Ala Leu Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly	
335 340 345	
aat gca att cct att ctt aat ata gat aat cca gct gaa aac ttc tat	1107
Asn Ala Ile Pro Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr	
350 355 360	
cca gca gaa gtt tct aat aat gga ttt cct atg att gta gct aat ttt	1155
Pro Ala Glu Val Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe	
365 370 375 380	
act ggt gtc cca ggt aaa aat aca gct gga tct gtt ggt gat gct acc	1203
Thr Gly Val Pro Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr	
385 390 395	
acc ttt ttt aca gaa att gac ttt ggt tta aaa gct act gat ctt gat	1251
Thr Phe Phe Thr Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp	

400	405	410	
aat aca tgg aag aat gca aat gaa cct ctt tct tct tta agc tat aaa Asn Thr Trp Lys Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys 415 420 425			1299
aaa aca cat aat cct atg gat gtc gca ggt ggt tgg aca gtt ggt ggg Lys Thr His Asn Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly 430 435 440			1347
tat aaa act cca gct cca tca gta act gaa ctt ggt atg gct cag ata Tyr Lys Thr Pro Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile 445 450 455 460			1395
ttg gaa aat cct gct ggg gta atg cca caa tat tat ttt ggt aac cct Leu Glu Asn Pro Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro 465 470 475			1443
aac tat gat aac aca gtt cca cag agt cca cca tat gta tat aaa aat Asn Tyr Asp Asn Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn 480 485 490			1491
gaa gct tct tat cag gct gca tat aag act gca tta act gcc gca ggt Glu Ala Ser Tyr Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly 495 500 505			1539
ggg acc gca gct gac att aaa aag gaa cat tgg cct cat aat gct gca Gly Thr Ala Ala Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala 510 515 520			1587
tca ggt ata tta gaa gct aat gat cca cca aat gtt aaa gac tta gct Ser Gly Ile Leu Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala 525 530 535 540			1635
aat atg aat gga aca cca aac cgc tta tca aat gcg ttt act aac tat Asn Met Asn Gly Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr 545 550 555			1683
gca ggt ggt agc tct aca aaa tct gca agt caa aat ggt tat ggt ttt Ala Gly Gly Ser Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe 560 565 570			1731
ggg gat tta atg aac tat agt gta aat gct gag gga gtg tta ttt gga Gly Asp Leu Met Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly 575 580 585			1779
gta tat tca aat gga gta caa ctt cca tta tat caa gta gct ctt tat Val Tyr Ser Asn Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr 590 595 600			1827
gat ttt aac tct aaa cag ggg tta cgt cgt gaa ggt ggt aac tta ttt Asp Phe Asn Ser Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe 605 610 615 620			1875
agt caa aca aga gaa tca ggg gac cca tct tca ggt gct gca aac act Ser Gln Thr Arg Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr 625 630 635			1923
tct ggg ttt ggt tca att aac gct aat act tta gaa gga tca aac gta Ser Gly Phe Gly Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val 640 645 650			1971
gat ata tct aca gag ttt gtc tca atg att gca aca caa cgt gga ttc Asp Ile Ser Thr Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe 655 660 665			2019

cag tca aat agt aaa att gta act act att gac caa atg tta gag aca 2067  
 Gln Ser Asn Ser Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr  
 670 675 680

gtt gta aat atg aag cgt tag 2088  
 Val Val Asn Met Lys Arg  
 685 690

<210> 2  
 <211> 690  
 <212> PRT  
 <213> *Lawsonia intracellularis*

<400> 2

Met Ser Leu Thr Ala Gly Met Trp Thr Gly Val Ser Gly Leu Leu Ser  
 1 5 10 15

His Gly Glu Lys Met Asn Val Ile Gly Asn Asn Ile Ala Asn Val Asn  
 20 25 30

Thr Val Gly Phe Lys Gly Gln Arg Met Asp Phe Ala Asp Phe Ile Tyr  
 35 40 45

Gln Asp Gly Phe Ser Thr Ala Gly Ile Thr Gln Ile Gly Arg Gly Val  
 50 55 60

Gly Ile Gly Ala Val Met Gly Asn Phe Gly Gln Gly Ser Phe Glu Thr  
 65 70 75 80

Thr Thr Glu Ala Thr Asp Leu Ala Ile Gly Gly Arg Gly Phe Phe Lys  
 85 90 95

Val Lys Pro Gln Gly Ser Glu Thr Ser Tyr Tyr Thr Arg Ala Gly Asn  
 100 105 110

Phe Arg Phe Asn Asn Asp Gly Tyr Leu Val Asp Pro His Gly Tyr Ala  
 115 120 125

Leu Gln Gly Trp Lys Ile Asp Asn Thr Glu Gly Pro Gln Arg Ile Ser  
 130 135 140

Gly Gly Val Asn Pro Gly Thr Asn Thr Ser Gln Ile Met Gly Thr Gly  
 145 150 155 160

Glu Pro Thr Asp Ile Arg Leu Asp Thr Trp Thr Val Ala Pro Leu Gln  
 165 170 175

Thr Thr Asn Val Ser Phe Asn Val Asn Leu Ser Ser Asp Lys Ser Gly  
 180 185 190

Asp Lys Ser Gln Asn Val Asn Ser Pro Phe Thr Ser Leu Phe Asn Ile  
 195 200 205  
 Trp Asn Gly Lys Gln Pro Ser Glu Pro Asn Asn Pro Pro Met Pro Glu  
 210 215 220  
 Ser Ala Tyr Ser Tyr Gln Thr Ser Ile Lys Val Tyr Asp Glu Ala Gly  
 225 230 235 240  
 Gly Thr His Thr Leu Thr Val Tyr Phe Asp Gln Val Ser Pro Lys Asp  
 245 250 255  
 Tyr Lys Gly Gly Gly Ser Gly Glu Ser Val Trp Glu Tyr Val Val Thr  
 260 265 270  
 Met Asp Pro Ser Glu Asp Asn Arg Gln Val Ser Val Gly Gly Asn Ile  
 275 280 285  
 Val Asp Ile Lys Asp Thr Lys Ala Ala Gly Met Leu Met Ser Gly Thr  
 290 295 300  
 Leu Ser Phe Asp Ser Ser Gly Lys Leu Ala Asn Gln Ser Ala Tyr Ser  
 305 310 315 320  
 Leu Asn Gly Ser Arg Lys Pro Ala Val Asp Pro Ala Thr Gly Ala Leu  
 325 330 335  
 Ile Asn Gly Asn Gly Phe Thr Ile Asp Arg Asp Gly Asn Ala Ile Pro  
 340 345 350  
 Ile Leu Asn Ile Asp Asn Pro Ala Glu Asn Phe Tyr Pro Ala Glu Val  
 355 360 365  
 Ser Asn Asn Gly Phe Pro Met Ile Val Ala Asn Phe Thr Gly Val Pro  
 370 375 380  
 Gly Lys Asn Thr Ala Gly Ser Val Gly Asp Ala Thr Thr Phe Phe Thr  
 385 390 395 400  
 Glu Ile Asp Phe Gly Leu Lys Ala Thr Asp Leu Asp Asn Thr Trp Lys  
 405 410 415  
 Asn Ala Asn Glu Pro Leu Ser Ser Leu Ser Tyr Lys Lys Thr His Asn  
 420 425 430  
 Pro Met Asp Val Ala Gly Gly Trp Thr Val Gly Gly Tyr Lys Thr Pro  
 435 440 445  
 Ala Pro Ser Val Thr Glu Leu Gly Met Ala Gln Ile Leu Glu Asn Pro

450                      455                      460  
 Ala Gly Val Met Pro Gln Tyr Tyr Phe Gly Asn Pro Asn Tyr Asp Asn  
 465                      470                      475                      480  
 Thr Val Pro Gln Ser Pro Pro Tyr Val Tyr Lys Asn Glu Ala Ser Tyr  
                     485                      490                      495  
 Gln Ala Ala Tyr Lys Thr Ala Leu Thr Ala Ala Gly Gly Thr Ala Ala  
                     500                      505                      510  
 Asp Ile Lys Lys Glu His Trp Pro His Asn Ala Ala Ser Gly Ile Leu  
                     515                      520                      525  
 Glu Ala Asn Asp Pro Pro Asn Val Lys Asp Leu Ala Asn Met Asn Gly  
                     530                      535                      540  
 Thr Pro Asn Arg Leu Ser Asn Ala Phe Thr Asn Tyr Ala Gly Gly Ser  
 545                      550                      555                      560  
 Ser Thr Lys Ser Ala Ser Gln Asn Gly Tyr Gly Phe Gly Asp Leu Met  
                     565                      570                      575  
 Asn Tyr Ser Val Asn Ala Glu Gly Val Leu Phe Gly Val Tyr Ser Asn  
                     580                      585                      590  
 Gly Val Gln Leu Pro Leu Tyr Gln Val Ala Leu Tyr Asp Phe Asn Ser  
                     595                      600                      605  
 Lys Gln Gly Leu Arg Arg Glu Gly Gly Asn Leu Phe Ser Gln Thr Arg  
                     610                      615                      620  
 Glu Ser Gly Asp Pro Ser Ser Gly Ala Ala Asn Thr Ser Gly Phe Gly  
 625                      630                      635                      640  
 Ser Ile Asn Ala Asn Thr Leu Glu Gly Ser Asn Val Asp Ile Ser Thr  
                     645                      650                      655  
 Glu Phe Val Ser Met Ile Ala Thr Gln Arg Gly Phe Gln Ser Asn Ser  
                     660                      665                      670  
 Lys Ile Val Thr Thr Ile Asp Gln Met Leu Glu Thr Val Val Asn Met  
                     675                      680                      685  
 Lys Arg  
                     690  
 <210> 3  
 <211> 751

&lt;212&gt; DNA

<213> *Lawsonia intracellularis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (32)..(715)

&lt;400&gt; 3

```

aagagttacc ctacgcttag gagctaacaa c atg ttt cgt atg att gtt ttt      52
                               Met Phe Arg Met Ile Val Phe
                               1         5

ttt act gta ggt atc att atg ctt att ctt gct tgc tta gct gca ctt      100
Phe Thr Val Gly Ile Ile Met Leu Ile Leu Ala Cys Leu Ala Ala Leu
          10          15          20

gag ttc ata caa gat ttt ccc aat agc tat caa gaa gat gga caa atg      148
Glu Phe Ile Gln Asp Phe Pro Asn Ser Tyr Gln Glu Asp Gly Gln Met
          25          30          35

gtt aca gga att att tca aaa ata ata ggc tct aac tgt gat aat tct      196
Val Thr Gly Ile Ile Ser Lys Ile Ile Gly Ser Asn Cys Asp Asn Ser
          40          45          50          55

tca aca tct gat ata aat aat aag aaa tcc ata gat aga gat aaa gat      244
Ser Thr Ser Asp Ile Asn Asn Lys Lys Ser Ile Asp Arg Asp Lys Asp
          60          65          70

aca tta ctc tca agt agt aat aga aat aca ata caa gcc ggt act cca      292
Thr Leu Leu Ser Ser Ser Asn Arg Asn Thr Ile Gln Ala Gly Thr Pro
          75          80          85

cat caa gaa aat aac ata aaa gaa gat ctt caa ctg act aac aaa aat      340
His Gln Glu Asn Asn Ile Lys Glu Asp Leu Gln Leu Thr Asn Lys Asn
          90          95          100

gaa caa aca act cca gaa gaa gaa gaa gaa agt aaa ttt att tgg tta      388
Glu Gln Thr Thr Pro Glu Glu Glu Glu Ser Lys Phe Ile Trp Leu
          105          110          115

aca gaa gct cca tca gag ctt aaa aaa gga gaa aaa gct ata aca caa      436
Thr Glu Ala Pro Ser Glu Leu Lys Lys Gly Glu Lys Ala Ile Thr Gln
          120          125          130          135

aca aga ttg tct att ggt aag gat ata tct ttt aga att act gct gat      484
Thr Arg Leu Ser Ile Gly Lys Asp Ile Ser Phe Arg Ile Thr Ala Asp
          140          145          150

gat gcc atc aaa gct caa tca atg atg tta aaa aat cca gat agg ttt      532
Asp Ala Ile Lys Ala Gln Ser Met Met Leu Lys Asn Pro Asp Arg Phe
          155          160          165

gtt tta gat ctt caa gga aag tgg ggt att tcc ctt cca cct att cca      580
Val Leu Asp Leu Gln Gly Lys Trp Gly Ile Ser Leu Pro Pro Ile Pro
          170          175          180

cct aca aat cct tgg tta aaa aaa ata cgc tta ggt act aat aat gga      628
Pro Thr Asn Pro Trp Leu Lys Lys Ile Arg Leu Gly Thr Asn Asn Gly
          185          190          195

aat aca cga ctt gtc ttt gat ctt caa aaa aaa cca tct aaa act gaa      676
Asn Thr Arg Leu Val Phe Asp Leu Gln Lys Lys Pro Ser Lys Thr Glu
          200          205          210          215

```

att aaa caa tta gat aca aat aaa att gaa atc caa att cattaattg 725  
 Ile Lys Gln Leu Asp Thr Asn Lys Ile Glu Ile Gln Ile  
 220 225

catattagac aataagttat aataaa 751

<210> 4  
 <211> 228  
 <212> PRT  
 <213> Lawsonia intracellularis

<400> 4

Met Phe Arg Met Ile Val Phe Phe Thr Val Gly Ile Ile Met Leu Ile  
 1 5 10 15

Leu Ala Cys Leu Ala Ala Leu Glu Phe Ile Gln Asp Phe Pro Asn Ser  
 20 25 30

Tyr Gln Glu Asp Gly Gln Met Val Thr Gly Ile Ile Ser Lys Ile Ile  
 35 40 45

Gly Ser Asn Cys Asp Asn Ser Ser Thr Ser Asp Ile Asn Asn Lys Lys  
 50 55 60

Ser Ile Asp Arg Asp Lys Asp Thr Leu Leu Ser Ser Ser Asn Arg Asn  
 65 70 75 80

Thr Ile Gln Ala Gly Thr Pro His Gln Glu Asn Asn Ile Lys Glu Asp  
 85 90 95

Leu Gln Leu Thr Asn Lys Asn Glu Gln Thr Thr Pro Glu Glu Glu Glu  
 100 105 110

Glu Ser Lys Phe Ile Trp Leu Thr Glu Ala Pro Ser Glu Leu Lys Lys  
 115 120 125

Gly Glu Lys Ala Ile Thr Gln Thr Arg Leu Ser Ile Gly Lys Asp Ile  
 130 135 140

Ser Phe Arg Ile Thr Ala Asp Asp Ala Ile Lys Ala Gln Ser Met Met  
 145 150 155 160

Leu Lys Asn Pro Asp Arg Phe Val Leu Asp Leu Gln Gly Lys Trp Gly  
 165 170 175

Ile Ser Leu Pro Pro Ile Pro Pro Thr Asn Pro Trp Leu Lys Lys Ile  
 180 185 190

Arg Leu Gly Thr Asn Asn Gly Asn Thr Arg Leu Val Phe Asp Leu Gln  
 195 200 205



Lys Lys Pro Ser Lys Thr Glu Ile Lys Gln Leu Asp Thr Asn Lys Ile  
 210 215 220

Glu Ile Gln Ile  
 225

<210> 5  
 <211> 1715  
 <212> DNA  
 <213> Lawsonia intracellularis

<220>  
 <221> CDS  
 <222> (34)..(1677)

<400> 5  
 aagcttttggt aatagtttct aaggagttat tta atg cat caa aaa agt tgt tta 54  
 Met His Gln Lys Ser Cys Leu  
 1 5

gtt gct tta tgt att atg ttt att att atg gtg caa gtt ctt cag gca 102  
 Val Ala Leu Cys Ile Met Phe Ile Ile Met Val Gln Val Leu Gln Ala  
 10 15 20

aat gca gct agc tat gtg gtt ttg cca ttt aaa gta aat gct cct cca 150  
 Asn Ala Ala Ser Tyr Val Val Leu Pro Phe Lys Val Asn Ala Pro Pro  
 25 30 35

agc tat act tat ttg gaa aaa gct atc cca tct atg tta act tct aga 198  
 Ser Tyr Thr Tyr Leu Glu Lys Ala Ile Pro Ser Met Leu Thr Ser Arg  
 40 45 50 55

ctt tat tgg gaa gaa cgt ttt caa cct atc ccg gat gct aat gct att 246  
 Leu Tyr Trp Glu Glu Arg Phe Gln Pro Ile Pro Asp Ala Asn Ala Ile  
 60 65 70

aaa gca gga aag gta gaa gat ata aag gaa atg gat aag gca agg ata 294  
 Lys Ala Gly Lys Val Glu Asp Ile Lys Glu Met Asp Lys Ala Arg Ile  
 75 80 85

gct aca ggt gca gac tat ctt ata tgg gga cag gta aat att gta ggt 342  
 Ala Thr Gly Ala Asp Tyr Leu Ile Trp Gly Gln Val Asn Ile Val Gly  
 90 95 100

gat gaa gct acg ctt gat gta caa gtt tgt gat ata gaa gga tca att 390  
 Asp Glu Ala Thr Leu Asp Val Gln Val Cys Asp Ile Glu Gly Ser Ile  
 105 110 115

tgg agg aaa agt aaa aat aca aaa gtt gat aat tta att act gcc ctt 438  
 Trp Arg Lys Ser Lys Asn Thr Lys Val Asp Asn Leu Ile Thr Ala Leu  
 120 125 130 135

caa gat aca gca gat gca att aat agt gag ttg ttt ggg cgt gca act 486  
 Gln Asp Thr Ala Asp Ala Ile Asn Ser Glu Leu Phe Gly Arg Ala Thr  
 140 145 150

aca aaa cca tca tca aaa gct act att gta gct caa atg aac tct gga 534  
 Thr Lys Pro Ser Ser Lys Ala Thr Ile Val Ala Gln Met Asn Ser Gly  
 155 160 165

ttg att aag gga aaa gga aat gaa aat cag tca tat ctt aat cca gaa 582

Leu Ile Lys Gly Lys Gly Asn Glu Asn Gln Ser Tyr Leu Asn Pro Glu	
170 175 180	
ttt cgt tat caa gga agc aat ctt tcc cgt ggc cga agt caa gct ctt	630
Phe Arg Tyr Gln Gly Ser Asn Leu Ser Arg Gly Arg Ser Gln Ala Leu	
185 190 195	
ccc ttt gct tca gtt ggt ata gtt gtt ggt gac ttt ata gga gat aat	678
Pro Phe Ala Ser Val Gly Ile Val Val Gly Asp Phe Ile Gly Asp Asn	
200 205 210 215	
aaa aat gaa gtt gcc ata tta agt gag tat aaa gtc cat att tat cga	726
Lys Asn Glu Val Ala Ile Leu Ser Glu Tyr Lys Val His Ile Tyr Arg	
220 225 230	
tgg gaa gaa gaa agg tta gct ctt ctt gga gaa tat aaa ttc cct cgc	774
Trp Glu Glu Arg Leu Ala Leu Leu Gly Glu Tyr Lys Phe Pro Arg	
235 240 245	
tca cta cag tct tta cat att cgt gct ttt gat gtg gat cat gat ggt	822
Ser Leu Gln Ser Leu His Ile Arg Ala Phe Asp Val Asp His Asp Gly	
250 255 260	
gta cag gaa atc att gtt tct tgc ttt gat cct tca tat gca aag cca	870
Val Gln Glu Ile Ile Val Ser Cys Phe Asp Pro Ser Tyr Ala Lys Pro	
265 270 275	
tat tgc ttt att ctt agt ttt aaa aat aga gtg ttt aaa gag tta gcc	918
Tyr Ser Phe Ile Leu Ser Phe Lys Asn Arg Val Phe Lys Glu Leu Ala	
280 285 290 295	
aca aac tta cca ttt tat tta aat gtg gtt aaa ctt cca cca gat ttt	966
Thr Asn Leu Pro Phe Tyr Leu Asn Val Val Lys Leu Pro Pro Asp Phe	
300 305 310	
tct cct atg tta att ggt caa aag agt gac aat tca agg att ttt tct	1014
Ser Pro Met Leu Ile Gly Gln Lys Ser Asp Asn Ser Arg Ile Phe Ser	
315 320 325	
ccc tct ggg gtt tat gaa ata gaa aaa cat gga cgt aac tat ata atg	1062
Pro Ser Gly Val Tyr Glu Ile Glu Lys His Gly Arg Asn Tyr Ile Met	
330 335 340	
gga aat cgt ctt agt ctt cca aag gaa gct aat att ttt aat ttt tct	1110
Gly Asn Arg Leu Ser Leu Pro Lys Glu Ala Asn Ile Phe Asn Phe Ser	
345 350 355	
tgg tta cca tca gat tca tta aaa gat gaa gaa gct aag tta gta ctt	1158
Trp Leu Pro Ser Asp Ser Leu Lys Asp Glu Glu Ala Lys Leu Val Leu	
360 365 370 375	
gta acc aat aat gaa aga tta gtt gta tat aat aca aaa ggt aca aga	1206
Val Thr Asn Asn Glu Arg Leu Val Val Tyr Asn Thr Lys Gly Thr Arg	
380 385 390	
ctt ttt atg act gaa gaa gtg tat tat ggt tct tct gtt ggt ata gac	1254
Leu Phe Met Thr Glu Glu Val Tyr Tyr Gly Ser Ser Val Gly Ile Asp	
395 400 405	
gag ccc agt aat atg cct ggt ctt gga aag tca aaa gag ctt atc cct	1302
Glu Pro Ser Asn Met Pro Gly Leu Gly Lys Ser Lys Glu Leu Ile Pro	
410 415 420	
tct aaa tat ttt atc cca gga cgg atg att cct att aat ctt gat tca	1350
Ser Lys Tyr Phe Ile Pro Gly Arg Met Ile Pro Ile Asn Leu Asp Ser	

425                      430                      435  
 atg ggg aaa tgg gag ttg ctt gta agc aag cca att tct gtt gca gca 1398  
 Met Gly Lys Trp Glu Leu Val Ser Lys Pro Ile Ser Val Ala Ala  
 440                      445                      450                      455  
 aaa ttt ttt gaa aat tat aga tct ttt gct gaa ggc gaa att cag gct 1446  
 Lys Phe Phe Glu Asn Tyr Arg Ser Phe Ala Glu Gly Glu Ile Gln Ala  
 460                      465                      470  
 tta aca tgg gac ggc tta gga tta ggt ctt gta tgg aat aca cgt cgt 1494  
 Leu Thr Trp Asp Gly Leu Gly Leu Gly Leu Val Trp Asn Thr Arg Arg  
 475                      480                      485  
 att aag gga act att aca gat ttt gcc tta gct gat atg aat aat gat 1542  
 Ile Lys Gly Thr Ile Thr Asp Phe Ala Leu Ala Asp Met Asn Asn Asp  
 490                      495                      500  
 ggg aag tta gac tta gtt gtt tcc gtt aat agc cat aca ggg att ctt 1590  
 Gly Lys Leu Asp Leu Val Val Ser Val Asn Ser His Thr Gly Ile Leu  
 505                      510                      515  
 gga cta gaa aaa cga aag aca att ata gta ttt tat cct tta gag gta 1638  
 Gly Leu Glu Lys Arg Lys Thr Ile Ile Val Phe Tyr Pro Leu Glu Val  
 520                      525                      530                      535  
 gat aaa caa ggt atc cct aag gct gtt gaa gat aac taa ttttttccta 1687  
 Asp Lys Gln Gly Ile Pro Lys Ala Val Glu Asp Asn  
 540                      545  
 ttaattattt ttttattctg atagttaa 1715  
  
 <210> 6  
 <211> 547  
 <212> PRT  
 <213> Lawsonia intracellularis  
  
 <400> 6  
  
 Met His Gln Lys Ser Cys Leu Val Ala Leu Cys Ile Met Phe Ile Ile  
 1                      5                      10                      15  
  
 Met Val Gln Val Leu Gln Ala Asn Ala Ala Ser Tyr Val Val Leu Pro  
 20                      25                      30  
  
 Phe Lys Val Asn Ala Pro Pro Ser Tyr Thr Tyr Leu Glu Lys Ala Ile  
 35                      40                      45  
  
 Pro Ser Met Leu Thr Ser Arg Leu Tyr Trp Glu Glu Arg Phe Gln Pro  
 50                      55                      60  
  
 Ile Pro Asp Ala Asn Ala Ile Lys Ala Gly Lys Val Glu Asp Ile Lys  
 65                      70                      75                      80  
  
 Glu Met Asp Lys Ala Arg Ile Ala Thr Gly Ala Asp Tyr Leu Ile Trp  
 85                      90                      95  
  
 Gly Gln Val Asn Ile Val Gly Asp Glu Ala Thr Leu Asp Val Gln Val

100	105	110
Cys Asp Ile Glu Gly Ser Ile Trp Arg Lys Ser Lys Asn Thr Lys Val		
115	120	125
Asp Asn Leu Ile Thr Ala Leu Gln Asp Thr Ala Asp Ala Ile Asn Ser		
130	135	140
Glu Leu Phe Gly Arg Ala Thr Thr Lys Pro Ser Ser Lys Ala Thr Ile		
145	150	155
Val Ala Gln Met Asn Ser Gly Leu Ile Lys Gly Lys Gly Asn Glu Asn		
165	170	175
Gln Ser Tyr Leu Asn Pro Glu Phe Arg Tyr Gln Gly Ser Asn Leu Ser		
180	185	190
Arg Gly Arg Ser Gln Ala Leu Pro Phe Ala Ser Val Gly Ile Val Val		
195	200	205
Gly Asp Phe Ile Gly Asp Asn Lys Asn Glu Val Ala Ile Leu Ser Glu		
210	215	220
Tyr Lys Val His Ile Tyr Arg Trp Glu Glu Glu Arg Leu Ala Leu Leu		
225	230	235
Gly Glu Tyr Lys Phe Pro Arg Ser Leu Gln Ser Leu His Ile Arg Ala		
245	250	255
Phe Asp Val Asp His Asp Gly Val Gln Glu Ile Ile Val Ser Cys Phe		
260	265	270
Asp Pro Ser Tyr Ala Lys Pro Tyr Ser Phe Ile Leu Ser Phe Lys Asn		
275	280	285
Arg Val Phe Lys Glu Leu Ala Thr Asn Leu Pro Phe Tyr Leu Asn Val		
290	295	300
Val Lys Leu Pro Pro Asp Phe Ser Pro Met Leu Ile Gly Gln Lys Ser		
305	310	315
Asp Asn Ser Arg Ile Phe Ser Pro Ser Gly Val Tyr Glu Ile Glu Lys		
325	330	335
His Gly Arg Asn Tyr Ile Met Gly Asn Arg Leu Ser Leu Pro Lys Glu		
340	345	350
Ala Asn Ile Phe Asn Phe Ser Trp Leu Pro Ser Asp Ser Leu Lys Asp		
355	360	365

Glu Glu Ala Lys Leu Val Leu Val Thr Asn Asn Glu Arg Leu Val Val  
 370 375 380  
 Tyr Asn Thr Lys Gly Thr Arg Leu Phe Met Thr Glu Glu Val Tyr Tyr  
 385 390 395 400  
 Gly Ser Ser Val Gly Ile Asp Glu Pro Ser Asn Met Pro Gly Leu Gly  
 405 410 415  
 Lys Ser Lys Glu Leu Ile Pro Ser Lys Tyr Phe Ile Pro Gly Arg Met  
 420 425 430  
 Ile Pro Ile Asn Leu Asp Ser Met Gly Lys Trp Glu Leu Leu Val Ser  
 435 440 445  
 Lys Pro Ile Ser Val Ala Ala Lys Phe Phe Glu Asn Tyr Arg Ser Phe  
 450 455 460  
 Ala Glu Gly Glu Ile Gln Ala Leu Thr Trp Asp Gly Leu Gly Leu Gly  
 465 470 475 480  
 Leu Val Trp Asn Thr Arg Arg Ile Lys Gly Thr Ile Thr Asp Phe Ala  
 485 490 495  
 Leu Ala Asp Met Asn Asn Asp Gly Lys Leu Asp Leu Val Val Ser Val  
 500 505 510  
 Asn Ser His Thr Gly Ile Leu Gly Leu Glu Lys Arg Lys Thr Ile Ile  
 515 520 525  
 Val Phe Tyr Pro Leu Glu Val Asp Lys Gln Gly Ile Pro Lys Ala Val  
 530 535 540  
 Glu Asp Asn  
 545

<210> 7  
 <211> 1564  
 <212> DNA  
 <213> Lawsonia intracellularis

<220>  
 <221> CDS  
 <222> (41)..(1522)

<400> 7  
 agaagtatgt tctataagta gagtaaggaa tataaaaaat atg gtt agt tat att 55  
 Met Val Ser Tyr Ile  
 1 5

cgt tta tta gga agt ata ttt tta gta tta gca att ttt ggt tgt ggc	103
Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala Ile Phe Gly Cys Gly	
10 15 20	
gct cag ttt aat aaa ccc tct tta ctt gat gaa acc cct ata gat tac	151
Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu Thr Pro Ile Asp Tyr	
25 30 35	
agt tct gta ctt tct gat tac ata gta gaa tta gaa aaa gaa cca ctt	199
Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu Glu Lys Glu Pro Leu	
40 45 50	
cag tat ata tta cta aaa aaa gaa aaa ttt tct caa atg gag ata tat	247
Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser Gln Met Glu Ile Tyr	
55 60 65	
aat tat caa ttc aca tca caa cat tgg tct cca gat aat ttt gta tca	295
Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro Asp Asn Phe Val Ser	
70 75 80 85	
cct gct ata tgg gaa cat cag gta gat ata tat atc cct cac cat cca	343
Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr Ile Pro His His Pro	
90 95 100	
gtt tca gaa cgt gca ctt ctt atc atc aat aat ggt att aat aat ggt	391
Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn Gly Ile Asn Asn Gly	
105 110 115	
aca ttt ttt act tct cct aaa gct cca act gat ttt act cca gaa gta	439
Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp Phe Thr Pro Glu Val	
120 125 130	
tta gaa gaa atc gct cgt tca aca aaa act gta gtc att gct cta agt	487
Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val Val Ile Ala Leu Ser	
135 140 145	
gat atc cca aat cag tat ctt act tat aga ggt gac tgg aga ttt ctt	535
Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly Asp Trp Arg Phe Leu	
150 155 160 165	
aag gaa gat gaa agt att gct atg agt tgg tct agt ttt tta caa gat	583
Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser Ser Phe Leu Gln Asp	
170 175 180	
cca gaa agt cgg tac aca aga cct ctc tat gtc cct atg gtt gca gca	631
Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val Pro Met Val Ala Ala	
185 190 195	
gtt tct cag gca atg act ctt gca gaa aag gag tta caa gca tta aaa	679
Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu Leu Gln Ala Leu Lys	
200 205 210	
att aag cat ttt att gta tct ggt gtg tca aag cgt gga tgg aca aca	727
Ile Lys His Phe Ile Val Ser Gly Val Ser Lys Arg Gly Trp Thr Thr	
215 220 225	
tgg ctt tca gct att gct gac tca cga gta gat gct att acc ccg ttt	775
Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp Ala Ile Thr Pro Phe	
230 235 240 245	
gtt att gat gca ttg aat act cgg aaa gtc ctt gga cat atg tat aaa	823
Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu Gly His Met Tyr Lys	
250 255 260	
aca tat gga aat aat tgg cct ata gca ttt tat cca tat tat aga ttt	871

Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr Pro Tyr Tyr Arg Phe	
265 270 275	
gat tta gat aaa caa cta gat aca gtt cct ttt ttc aat ctt atg aat	919
Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe Phe Asn Leu Met Asn	
280 285 290	
att gtt gat cca tat aga tat tta gga aca cca tat aag tct cga ctt	967
Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro Tyr Lys Ser Arg Leu	
295 300 305	
gct atc cct aaa tat att gta aat gca agt gga gat gat ttt tat gtc	1015
Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly Asp Asp Phe Tyr Val	
310 315 320 325	
cct gat aat tca agt ttt tac tat gat gat ctc cct gga gag aaa gca	1063
Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asn Leu Pro Gly Glu Lys Ala	
330 335 340	
tta cgt ttt gca cca aac tca aat cat cat ggg ata tta aat ttc aca	1111
Leu Arg Phe Ala Pro Asn Ser Asn His His Gly Ile Leu Asn Phe Thr	
345 350 355	
aaa caa tcg ctt att cct ttt gtg aat aga gta caa aaa ggt att tca	1159
Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val Gln Lys Gly Ile Ser	
360 365 370	
acg cca gtt tta gat att tcc aca gag atg acg gaa cga gtt caa tat	1207
Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr Glu Arg Val Gln Tyr	
375 380 385	
gtg act gtt cgt ttt tct gaa gtt cca gag aag ata gta ctt tgg aaa	1255
Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys Ile Val Leu Trp Lys	
390 395 400 405	
gca gca aat cca gag tca cga gat ttt cgt tat gcc tgt cgt gtt agg	1303
Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr Ala Cys Arg Val Arg	
410 415 420	
tac atg gaa aca cca tta cac ctt tct gca aca ggg gaa gtt agc gtt	1351
Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr Gly Glu Val Ser Val	
425 430 435	
tca tta gag atc cct tct gta gga tgg caa gct gct ttt att gaa gct	1399
Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala Ala Phe Ile Glu Ala	
440 445 450	
aca ttt aaa gat ggt ttt gtt gca aca aca cca gtg tat att tta cca	1447
Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro Val Tyr Ile Leu Pro	
455 460 465	
aaa gat ata tat cca cct ata aaa ata cca cct gta cat gga tta tta	1495
Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro Val His Gly Leu Leu	
470 475 480 485	
tgt aag ttt gta cat ggt cga acc tag taactagtag ttgttgtagt	1542
Cys Lys Phe Val His Gly Arg Thr	
490	
gataatctaa aaggatatag at	1564
<210> 8	
<211> 493	
<212> PRT	

&lt;213&gt; Lawsonia intracellularis

&lt;400&gt; 8

Met Val Ser Tyr Ile Arg Leu Leu Gly Ser Ile Phe Leu Val Leu Ala  
 1 5 10 15

Ile Phe Gly Cys Gly Ala Gln Phe Asn Lys Pro Ser Leu Leu Asp Glu  
 20 25 30

Thr Pro Ile Asp Tyr Ser Ser Val Leu Ser Asp Tyr Ile Val Glu Leu  
 35 40 45

Glu Lys Glu Pro Leu Gln Tyr Ile Leu Leu Lys Lys Glu Lys Phe Ser  
 50 55 60

Gln Met Glu Ile Tyr Asn Tyr Gln Phe Thr Ser Gln His Trp Ser Pro  
 65 70 75 80

Asp Asn Phe Val Ser Pro Ala Ile Trp Glu His Gln Val Asp Ile Tyr  
 85 90 95

Ile Pro His His Pro Val Ser Glu Arg Ala Leu Leu Ile Ile Asn Asn  
 100 105 110

Gly Ile Asn Asn Gly Thr Phe Phe Thr Ser Pro Lys Ala Pro Thr Asp  
 115 120 125

Phe Thr Pro Glu Val Leu Glu Glu Ile Ala Arg Ser Thr Lys Thr Val  
 130 135 140

Val Ile Ala Leu Ser Asp Ile Pro Asn Gln Tyr Leu Thr Tyr Arg Gly  
 145 150 155 160

Asp Trp Arg Phe Leu Lys Glu Asp Glu Ser Ile Ala Met Ser Trp Ser  
 165 170 175

Ser Phe Leu Gln Asp Pro Glu Ser Arg Tyr Thr Arg Pro Leu Tyr Val  
 180 185 190

Pro Met Val Ala Ala Val Ser Gln Ala Met Thr Leu Ala Glu Lys Glu  
 195 200 205

Leu Gln Ala Leu Lys Ile Lys His Phe Ile Val Ser Gly Val Ser Lys  
 210 215 220

Arg Gly Trp Thr Thr Trp Leu Ser Ala Ile Ala Asp Ser Arg Val Asp  
 225 230 235 240

Ala Ile Thr Pro Phe Val Ile Asp Ala Leu Asn Thr Arg Lys Val Leu



	245		250		255
Gly His Met Tyr Lys Thr Tyr Gly Asn Asn Trp Pro Ile Ala Phe Tyr	260		265		270
Pro Tyr Tyr Arg Phe Asp Leu Asp Lys Gln Leu Asp Thr Val Pro Phe	275		280		285
Phe Asn Leu Met Asn Ile Val Asp Pro Tyr Arg Tyr Leu Gly Thr Pro	290		295		300
Tyr Lys Ser Arg Leu Ala Ile Pro Lys Tyr Ile Val Asn Ala Ser Gly	305		310		315
Asp Asp Phe Tyr Val Pro Asp Asn Ser Ser Phe Tyr Tyr Asp Asp Leu	325		330		335
Pro Gly Glu Lys Ala Leu Arg Phe Ala Pro Asn Ser Asn His His Gly	340		345		350
Ile Leu Asn Phe Thr Lys Gln Ser Leu Ile Pro Phe Val Asn Arg Val	355		360		365
Gln Lys Gly Ile Ser Thr Pro Val Leu Asp Ile Ser Thr Glu Met Thr	370		375		380
Glu Arg Val Gln Tyr Val Thr Val Arg Phe Ser Glu Val Pro Glu Lys	385		390		395
Ile Val Leu Trp Lys Ala Ala Asn Pro Glu Ser Arg Asp Phe Arg Tyr	405		410		415
Ala Cys Arg Val Arg Tyr Met Glu Thr Pro Leu His Leu Ser Ala Thr	420		425		430
Gly Glu Val Ser Val Ser Leu Glu Ile Pro Ser Val Gly Trp Gln Ala	435		440		445
Ala Phe Ile Glu Ala Thr Phe Lys Asp Gly Phe Val Ala Thr Thr Pro	450		455		460
Val Tyr Ile Leu Pro Lys Asp Ile Tyr Pro Pro Ile Lys Ile Pro Pro	465		470		475
Val His Gly Leu Leu Cys Lys Phe Val His Gly Arg Thr	485		490		

&lt;210&gt; 9

&lt;211&gt; 2096

&lt;212&gt; DNA

<213> *Lawsonia intracellularis*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (12) .. (2096)

&lt;400&gt; 9

```

aggacaaaac t atg gcg gat tat ctt tca gga gga att tct ttt gga gga      50
          Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly
            1             5             10

att ggt agt gga acc gat ttc caa gct atg att gat caa ctt aag aaa      98
Ile Gly Ser Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys
   15             20             25

att gag ctt att cct aaa aat aga ctt gta gtt tcc cat gaa caa tgg     146
Ile Glu Leu Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp
   30             35             40             45

aca aaa aaa tat aaa gca ttt gaa gag ctt ata aaa aca gtt aaa gat     194
Thr Lys Lys Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp
            50             55             60

act gaa gcg tct tta agt aag cta agt tct gtt ggt gct att tta aaa     242
Thr Glu Ala Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys
            65             70             75

aaa gaa ggt tct gtt tca aat act tct gtt gca agc gtt aag gca agt     290
Lys Glu Gly Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser
            80             85             90

tct gat gca tct gat gga aca cat aca att gat gtg aaa cag ctt gca     338
Ser Asp Ala Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala
            95             100             105

aca aac acg att ctt tct aat aat cat att ttt gat tct aaa act gaa     386
Thr Asn Thr Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu
   110             115             120             125

agt att aat aat aca ggt tca cct ggt atc ttt gct tat gag tat aaa     434
Ser Ile Asn Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys
            130             135             140

ggg gaa cta cat gaa gtt gaa gtt cct cca ggt agt gat ctt gaa tat     482
Gly Glu Leu His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr
            145             150             155

ctt gca aca tta ata aac aaa gat tct aat aat cct ggt gtt aaa gca     530
Leu Ala Thr Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala
            160             165             170

aac ctt atc aag act ggc gat ggc tat atg ttt agt ctt gaa gga act     578
Asn Leu Ile Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr
            175             180             185

gaa act ggt gca aat gcg act tta tct att tca aat aag aca acg ctt     626
Glu Thr Gly Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu
   190             195             200             205

cca gac ttt aaa gca tct gtt gct acc agc agt gca tta gct aat ggt     674
Pro Asp Phe Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly
            210             215             220

```

gaa gat aca att att aat act tca gga aca act caa caa ttt tct ttt Glu Asp Thr Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe 225 230 235	722
gaa tac aat gga aga aca ttt act ttc gat att cct tca gga aca aca Glu Tyr Asn Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr 240 245 250	770
gca aaa gaa ctc caa aca gct ata aat gaa aat aca aaa aat aca gga Ala Lys Glu Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly 255 260 265	818
gta cgt gca act ttt gaa aaa cat ggc tca gat ata gta ttg caa tta Val Arg Ala Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu 270 275 280 285	866
gaa gga aca gtt cct aat caa caa gtt aaa gta acc gct agc cct act Glu Gly Thr Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr 290 295 300	914
gat ctt gga agt ttc aca tct tcg ggt caa gca ggc tgg aat aaa cgt Asp Leu Gly Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg 305 310 315	962
gat tct caa gat gct att ttt aat att aat ggt tgg gac caa gaa ctt Asp Ser Gln Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu 320 325 330	1010
aca tct tct aca aat gaa ctt aca gaa gtt atc cca gga ctt caa att Thr Ser Ser Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile 335 340 345	1058
aca cta ctt tcc gaa ggg aaa aca caa att aca att cag act tct act Thr Leu Leu Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr 350 355 360 365	1106
gac gaa gta aaa aaa caa gtt gag aaa gca gta gag tct ata aat aat Asp Glu Val Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn 370 375 380	1154
gtt ctt tcc aaa att caa gag tta act aaa gca aca gct gaa gac aaa Val Leu Ser Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys 385 390 395	1202
gat gat agt aaa gac act tct agt tct tca agt aaa att cca tca tat Asp Asp Ser Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr 400 405 410	1250
tta caa agt cct aca aaa gtg aag gct gga cta ttt aca ggt gat act Leu Gln Ser Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr 415 420 425	1298
ggc ata caa atg ctt agt act aga ctt aag tct atc ttt tct tct aat Gly Ile Gln Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn 430 435 440 445	1346
ggt cta ggt ttt tct cct aaa caa aca caa gat ggt cca ggg gat cta Gly Leu Gly Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu 450 455 460	1394
ttt tca tca ctt gct tca att ggt att gtc gta gat gct gat gag ggt Phe Ser Ser Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly 465 470 475	1442
agt gaa act ttt gga caa ctt aaa att tta gat aga gaa aca att ggt	1490

Ser Glu Thr Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly  
 480 485 490  
 cct gat gca cct tat aca act ctt gat gag gca tta aaa aaa gat cca 1538  
 Pro Asp Ala Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro  
 495 500 505  
 caa gca gta gca gat ata tta gct ggt agt tct gga ata tct gat tca 1586  
 Gln Ala Val Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser  
 510 515 520 525  
 aca gat ttt tct tat caa gat cat att gtt gga aaa aca caa gct ggt 1634  
 Thr Asp Phe Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly  
 530 535 540  
 aca tat gat gta aag tat tct gta gat gca agt ggt act ata gga gac 1682  
 Thr Tyr Asp Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp  
 545 550 555  
 gtt tac att gga ggt gta aaa gct tct cta tct gat cct gca aaa aat 1730  
 Val Tyr Ile Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn  
 560 565 570  
 ata tat acg gtc aca tct ggt cct gct aca ggt ctt agt ata gca gtt 1778  
 Ile Tyr Thr Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val  
 575 580 585  
 aat aat cgt act cca ggt atc aat gta gaa agt act gta aga gtc aaa 1826  
 Asn Asn Arg Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys  
 590 595 600 605  
 caa ggt aaa ctt agc caa ata caa gaa gca ctt aaa gct gaa gta cag 1874  
 Gln Gly Lys Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln  
 610 615 620  
 caa gat cct tta aaa gaa aac aca ggt cct tta att atc atg caa gat 1922  
 Gln Asp Pro Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp  
 625 630 635  
 aac tat aag gat gtt atg aaa aat ctt gag aca aga ata gaa aaa gaa 1970  
 Asn Tyr Lys Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu  
 640 645 650  
 aca caa aga gtt act agt tgg gaa cgt atg atg cgt tta aaa ttt tct 2018  
 Thr Gln Arg Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser  
 655 660 665  
 aga ctt gat gct gta tta gca aaa tat aat cag atg atg tca gca aat 2066  
 Arg Leu Asp Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn  
 670 675 680 685  
 gct tct agt tta ggg caa ctt ggt gca taa 2096  
 Ala Ser Ser Leu Gly Gln Leu Gly Ala  
 690

<210> 10  
 <211> 694  
 <212> PRT  
 <213> Lawsonia intracellularis

<400> 10

Met Ala Asp Tyr Leu Ser Gly Gly Ile Ser Phe Gly Gly Ile Gly Ser  
 1 5 10 15

Gly Thr Asp Phe Gln Ala Met Ile Asp Gln Leu Lys Lys Ile Glu Leu  
                   20                  25                  30  
 Ile Pro Lys Asn Arg Leu Val Val Ser His Glu Gln Trp Thr Lys Lys  
                   35                  40                  45  
 Tyr Lys Ala Phe Glu Glu Leu Ile Lys Thr Val Lys Asp Thr Glu Ala  
                   50                  55                  60  
 Ser Leu Ser Lys Leu Ser Ser Val Gly Ala Ile Leu Lys Lys Glu Gly  
                   65                  70                  75                  80  
 Ser Val Ser Asn Thr Ser Val Ala Ser Val Lys Ala Ser Ser Asp Ala  
                   85                  90                  95  
 Ser Asp Gly Thr His Thr Ile Asp Val Lys Gln Leu Ala Thr Asn Thr  
                   100                  105                  110  
 Ile Leu Ser Asn Asn His Ile Phe Asp Ser Lys Thr Glu Ser Ile Asn  
                   115                  120                  125  
 Asn Thr Gly Ser Pro Gly Ile Phe Ala Tyr Glu Tyr Lys Gly Glu Leu  
                   130                  135                  140  
 His Glu Val Glu Val Pro Pro Gly Ser Asp Leu Glu Tyr Leu Ala Thr  
                   145                  150                  155                  160  
 Leu Ile Asn Lys Asp Ser Asn Asn Pro Gly Val Lys Ala Asn Leu Ile  
                   165                  170                  175  
 Lys Thr Gly Asp Gly Tyr Met Phe Ser Leu Glu Gly Thr Glu Thr Gly  
                   180                  185                  190  
 Ala Asn Ala Thr Leu Ser Ile Ser Asn Lys Thr Thr Leu Pro Asp Phe  
                   195                  200                  205  
 Lys Ala Ser Val Ala Thr Ser Ser Ala Leu Ala Asn Gly Glu Asp Thr  
                   210                  215                  220  
 Ile Ile Asn Thr Ser Gly Thr Thr Gln Gln Phe Ser Phe Glu Tyr Asn  
                   225                  230                  235                  240  
 Gly Arg Thr Phe Thr Phe Asp Ile Pro Ser Gly Thr Thr Ala Lys Glu  
                   245                  250                  255  
 Leu Gln Thr Ala Ile Asn Glu Asn Thr Lys Asn Thr Gly Val Arg Ala  
                   260                  265                  270

Thr Phe Glu Lys His Gly Ser Asp Ile Val Leu Gln Leu Glu Gly Thr  
 275 280 285

Val Pro Asn Gln Gln Val Lys Val Thr Ala Ser Pro Thr Asp Leu Gly  
 290 295 300

Ser Phe Thr Ser Ser Gly Gln Ala Gly Trp Asn Lys Arg Asp Ser Gln  
 305 310 315 320

Asp Ala Ile Phe Asn Ile Asn Gly Trp Asp Gln Glu Leu Thr Ser Ser  
 325 330 335

Thr Asn Glu Leu Thr Glu Val Ile Pro Gly Leu Gln Ile Thr Leu Leu  
 340 345 350

Ser Glu Gly Lys Thr Gln Ile Thr Ile Gln Thr Ser Thr Asp Glu Val  
 355 360 365

Lys Lys Gln Val Glu Lys Ala Val Glu Ser Ile Asn Asn Val Leu Ser  
 370 375 380

Lys Ile Gln Glu Leu Thr Lys Ala Thr Ala Glu Asp Lys Asp Asp Ser  
 385 390 395 400

Lys Asp Thr Ser Ser Ser Ser Ser Lys Ile Pro Ser Tyr Leu Gln Ser  
 405 410 415

Pro Thr Lys Val Lys Ala Gly Leu Phe Thr Gly Asp Thr Gly Ile Gln  
 420 425 430

Met Leu Ser Thr Arg Leu Lys Ser Ile Phe Ser Ser Asn Gly Leu Gly  
 435 440 445

Phe Ser Pro Lys Gln Thr Gln Asp Gly Pro Gly Asp Leu Phe Ser Ser  
 450 455 460

Leu Ala Ser Ile Gly Ile Val Val Asp Ala Asp Glu Gly Ser Glu Thr  
 465 470 475 480

Phe Gly Gln Leu Lys Ile Leu Asp Arg Glu Thr Ile Gly Pro Asp Ala  
 485 490 495

Pro Tyr Thr Thr Leu Asp Glu Ala Leu Lys Lys Asp Pro Gln Ala Val  
 500 505 510

Ala Asp Ile Leu Ala Gly Ser Ser Gly Ile Ser Asp Ser Thr Asp Phe  
 515 520 525

Ser Tyr Gln Asp His Ile Val Gly Lys Thr Gln Ala Gly Thr Tyr Asp  
 530 535 540

Val Lys Tyr Ser Val Asp Ala Ser Gly Thr Ile Gly Asp Val Tyr Ile  
 545 550 555 560

Gly Gly Val Lys Ala Ser Leu Ser Asp Pro Ala Lys Asn Ile Tyr Thr  
 565 570 575

Val Thr Ser Gly Pro Ala Thr Gly Leu Ser Ile Ala Val Asn Asn Arg  
 580 585 590

Thr Pro Gly Ile Asn Val Glu Ser Thr Val Arg Val Lys Gln Gly Lys  
 595 600 605

Leu Ser Gln Ile Gln Glu Ala Leu Lys Ala Glu Val Gln Gln Asp Pro  
 610 615 620

Leu Lys Glu Asn Thr Gly Pro Leu Ile Ile Met Gln Asp Asn Tyr Lys  
 625 630 635 640

Asp Val Met Lys Asn Leu Glu Thr Arg Ile Glu Lys Glu Thr Gln Arg  
 645 650 655

Val Thr Ser Trp Glu Arg Met Met Arg Leu Lys Phe Ser Arg Leu Asp  
 660 665 670

Ala Val Leu Ala Lys Tyr Asn Gln Met Met Ser Ala Asn Ala Ser Ser  
 675 680 685

Leu Gly Gln Leu Gly Ala  
 690

<210> 11  
 <211> 1200  
 <212> DNA  
 <213> *Lawsonia intracellularis*

<220>  
 <221> CDS  
 <222> (13)..(1200)

<400> 11  
 taggagatag tt atg gct aat gtt agt gga atc cct gca cca cga tta ctt 51  
 Met Ala Asn Val Ser Gly Ile Pro Ala Pro Arg Leu Leu  
 1 5 10

tcc aca aca aat caa atg acc aat gca gct gct ggt aat ac~~t~~ aat aga 99  
 Ser Thr Thr Asn Gln Met Thr Asn Ala Ala Gly Asn Thr Asn Arg  
 15 20 25

gct acc ggt agt atg aac ggt cgt aat ctc aca caa ata aa~~a~~ aca cct 147  
 Ala Thr Gly Ser Met Asn Gly Arg Asn Leu Thr Gln Ile Lys Thr Pro

30	35	40	45	
cag tcc atg att gat aat gct tca gaa gaa tta aca act tct ctt gaa				195
Gln Ser Met Ile Asp Asn Ala Ser Glu Glu Leu Thr Thr Ser Leu Glu	50	55	60	
tct aaa agc agt gac gac ttt gca att aaa gat cgt aaa aga caa ggg				243
Ser Lys Ser Ser Asp Asp Phe Ala Ile Lys Asp Arg Lys Arg Gln Gly	65	70	75	
aaa gga tct gat tct cta tta aaa atg gtt caa gaa tat aca gag ctg				291
Lys Gly Ser Asp Ser Leu Leu Lys Met Val Gln Glu Tyr Thr Glu Leu	80	85	90	
acg aat gat gat acc cgt aat gct aaa aga gct atg tta tcc cag gta				339
Thr Asn Asp Asp Thr Arg Asn Ala Lys Arg Ala Met Leu Ser Gln Val	95	100	105	
tta cgt gca agt caa agt tca caa gat gta ctc gaa aaa aca tta gaa				387
Leu Arg Ala Ser Gln Ser Ser Gln Asp Val Leu Glu Lys Thr Leu Glu	110	115	120	125
caa ttt tct aat aaa aca gat gct tgg gct tct ctt gca gaa att gca				435
Gln Phe Ser Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala	130	135	140	
caa gaa tat ggt gca gaa tct cca cag cca aca gga tta aaa tct gta				483
Gln Glu Tyr Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val	145	150	155	
tta gat gct atg gag aca tta gaa aat gag ttt ggt gat gaa att aaa				531
Leu Asp Ala Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys	160	165	170	
gca gga cta aaa gga gct cta aat tca aaa gaa ttt act gat ata ggc				579
Ala Gly Leu Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly	175	180	185	
agt gca gca cag tta aga gat ctt tat aca aca aca gta act ata aca				627
Ser Ala Ala Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr	190	195	200	205
gct gca cct gat gca gtg tta gca aga ctt ctt gaa gaa tat gag agt				675
Ala Ala Pro Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser	210	215	220	
gat gat gat ctg gat aga gcc att gat ttc ctt cta tct aca ctt ggt				723
Asp Asp Asp Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly	225	230	235	
gga gag ctt gaa tca gct gat cca agt atg gat aaa gta cat ctt Caa				771
Gly Glu Leu Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln	240	245	250	
agt gta atg ggt gat att gaa aaa aca caa caa ctt cat agc tct cat				819
Ser Val Met Gly Asp Ile Glu Lys Thr Gln Gln His Ser Ser His	255	260	265	
aaa caa tgt act aca gcc ctt agc agg tgg aaa gag aaa cat aaa ggt				867
Lys Gln Cys Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly	270	275	280	285
ggg ggg gaa aat agt aca cta act cct tta gaa atg atg cgt gaa cta				915
Gly Gly Glu Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu	290	295	300	



att gca cta aaa aat gaa aat ttt att tct cct tcc tct ata gat aaa 963  
 ile ala leu lys asn glu asn phe ile ser pro ser ser ile asp lys  
                   305                  310                  315

att gtt gat caa gct gat ccc caa gat att gaa aaa gaa gtc ctt ttt 1011  
 ile val asp gln ala asp pro gln asp ile glu lys glu val leu phe  
                   320                  325                  330

tta caa gag atg tta gct gct gta aga aaa ttt ccc att atg gta ttt 1059  
 leu gln glu met leu ala ala val arg lys phe pro ile met val phe  
                   335                  340                  345

gat aat gtc gaa aat cgt gta aga gtt atg ggt gct gta caa gat gct 1107  
 asp asn val glu asn arg val arg val met gly ala val gln asp ala  
                   350                  355                  360                  365

gtt gac gat gct gta aga aga gaa gat gaa ttc ctc ttt caa aaa gaa 1155  
 val asp asp ala val arg arg glu asp glu phe leu phe gln lys glu  
                   370                  375                  380

cat cct gat gta cca cta caa cca gat gaa aat aat ata caa taa 1200  
 his pro asp val pro leu gln pro asp glu asn asn ile gln  
                   385                  390                  395

<210> 12  
 <211> 395  
 <212> PRT  
 <213> Lawsonia intracellularis

<400> 12

Met ala asn val ser gly ile pro ala pro arg leu leu ser thr thr  
 1                  5                  10                  15

asn gln met thr asn ala ala ala gly asn thr asn arg ala thr gly  
                   20                  25                  30

ser met asn gly arg asn leu thr gln ile lys thr pro gln ser met  
                   35                  40                  45

ile asp asn ala ser glu glu leu thr thr ser leu glu ser lys ser  
                   50                  55                  60

ser asp asp phe ala ile lys asp arg lys arg gln gly lys gly ser  
                   65                  70                  75                  80

asp ser leu leu lys met val gln glu tyr thr glu leu thr asn asp  
                   85                  90                  95

asp thr arg asn ala lys arg ala met leu ser gln val leu arg ala  
                   100                  105                  110

ser gln ser ser gln asp val leu glu lys thr leu glu gln phe ser  
                   115                  120                  125

Asn Lys Thr Asp Ala Trp Ala Ser Leu Ala Glu Ile Ala Gln Glu Tyr  
 130 135 140

Gly Ala Glu Ser Pro Gln Pro Thr Gly Leu Lys Ser Val Leu Asp Ala  
 145 150 155 160

Met Glu Thr Leu Glu Asn Glu Phe Gly Asp Glu Ile Lys Ala Gly Leu  
 165 170 175

Lys Gly Ala Leu Asn Ser Lys Glu Phe Thr Asp Ile Gly Ser Ala Ala  
 180 185 190

Gln Leu Arg Asp Leu Tyr Thr Thr Thr Val Thr Ile Thr Ala Ala Pro  
 195 200 205

Asp Ala Val Leu Ala Arg Leu Leu Glu Glu Tyr Glu Ser Asp Asp Asp  
 210 215 220

Leu Asp Arg Ala Ile Asp Phe Leu Leu Ser Thr Leu Gly Gly Glu Leu  
 225 230 235 240

Glu Ser Ala Asp Pro Ser Met Asp Lys Val His Leu Gln Ser Val Met  
 245 250 255

Gly Asp Ile Glu Lys Thr Gln Gln Leu His Ser Ser His Lys Gln Cys  
 260 265 270

Thr Thr Ala Leu Ser Arg Trp Lys Glu Lys His Lys Gly Gly Gly Glu  
 275 280 285

Asn Ser Thr Leu Thr Pro Leu Glu Met Met Arg Glu Leu Ile Ala Leu  
 290 295 300

Lys Asn Glu Asn Phe Ile Ser Pro Ser Ser Ile Asp Lys Ile Val Asp  
 305 310 315 320

Gln Ala Asp Pro Gln Asp Ile Glu Lys Glu Val Leu Phe Leu Gln Glu  
 325 330 335

Met Leu Ala Ala Val Arg Lys Phe Pro Ile Met Val Phe Asp Asn Val  
 340 345 350

Glu Asn Arg Val Arg Val Met Gly Ala Val Gln Asp Ala Val Asp Asp  
 355 360 365

Ala Val Arg Arg Glu Asp Glu Phe Leu Phe Gln Lys Glu His Pro Asp  
 370 375 380

Val Pro Leu Gln Pro Asp Glu Asn Asn Ile Gln

```

385                               390                               395

<210> 13
<211> 1269
<212> DNA
<213> Lawsonia intracellularis

<220>
<221> CDS
<222> (32)..(1222)

<400> 13
tgttggaaat tctctctgga ggagtaaagc a atg aca aat ttt gga gat ata      52
                               Met Thr Asn Phe Gly Asp Ile
                               1                               5

agc gga agc tcc gca aga atg agt agc ttg atg act ggt aca tcc ggt      100
Ser Gly Ser Ser Ala Arg Met Ser Ser Leu Met Thr Gly Thr Ser Gly
      10                               15                               20

gaa gaa gga ctt gaa gaa ctt gaa ggt ggt gtt cct aaa gag caa ggt      148
Glu Glu Gly Leu Glu Glu Leu Glu Gly Gly Val Pro Lys Glu Gln Gly
      25                               30                               35

ggt cca ggt aaa gga gat gct tca gag gct gct aaa ggt caa gca gca      196
Gly Pro Gly Lys Gly Asp Ala Ser Glu Ala Ala Lys Gly Gln Ala Ala
      40                               45                               50                               55

gca gat agt att aat tca gct ggt ggt act gaa aag cct gga gaa gtt      244
Ala Asp Ser Ile Asn Ser Ala Gly Gly Thr Glu Lys Pro Gly Glu Val
      60                               65                               70

ggt gat aag gaa gat gta ggg gaa ggt ggc gaa ata cct gaa ggt ggt      292
Gly Asp Lys Glu Asp Val Gly Glu Gly Gly Glu Ile Pro Glu Gly Gly
      75                               80                               85

gaa ata cct gag ggt ggt gaa gaa gtt cca gag gaa ccc cca tat gtc      340
Glu Ile Pro Glu Gly Gly Glu Glu Val Pro Glu Glu Pro Pro Tyr Val
      90                               95                               100

cct cct cca ttg gtt gaa cca gct aaa atc agt aca gta aca gat ctc      388
Pro Pro Pro Leu Val Glu Pro Ala Lys Ile Ser Thr Val Thr Asp Leu
      105                               110                               115

agt acg tta atg gga tca cta cag ctg aca gag caa aaa aag aat gct      436
Ser Thr Leu Met Gly Ser Leu Gln Leu Thr Glu Gln Lys Lys Asn Ala
      120                               125                               130                               135

gaa aaa aca gta aat gaa att aaa gca cag aat aaa gag caa caa gta      484
Glu Lys Thr Val Asn Glu Ile Lys Ala Gln Asn Lys Glu Gln Gln Val
      140                               145                               150

aag ttc caa gag caa att aaa aag att gag gat aat att gct gaa tct      532
Lys Phe Gln Glu Ile Lys Lys Ile Glu Asp Asn Ile Ala Glu Ser
      155                               160                               165

aag aaa agt ggt ata ctt aag ttt ttc caa aag ttg ttt gca gtt att      580
Lys Lys Ser Gly Ile Leu Lys Phe Phe Gln Lys Leu Phe Ala Val Ile
      170                               175                               180

ggt gct gta cta gga gct att gga ggt gcg cta gct att gct gca ggt      628
Gly Ala Val Leu Gly Ala Ile Gly Gly Ala Leu Ala Ile Ala Ala Gly
      185                               190                               195

```



Leu Met Thr Gly Thr Ser Gly Glu Glu Gly Leu Glu Glu Leu Glu Gly  
                   20                                  25                                  30

Gly Val Pro Lys Glu Gln Gly Gly Pro Gly Lys Gly Asp Ala Ser Glu  
                   35                                  40                                  45

Ala Ala Lys Gly Gln Ala Ala Ala Asp Ser Ile Asn Ser Ala Gly Gly  
           50                                  55                                  60

Thr Glu Lys Pro Gly Glu Val Gly Asp Lys Glu Asp Val Gly Glu Gly  
 65                                  70                                  75                                  80

Gly Glu Ile Pro Glu Gly Gly Glu Ile Pro Glu Gly Gly Glu Glu Val  
                                   85                                  90                                  95

Pro Glu Glu Pro Pro Tyr Val Pro Pro Pro Leu Val Glu Pro Ala Lys  
                   100                                  105                                  110

Ile Ser Thr Val Thr Asp Leu Ser Thr Leu Met Gly Ser Leu Gln Leu  
           115                                  120                                  125

Thr Glu Gln Lys Lys Asn Ala Glu Lys Thr Val Asn Glu Ile Lys Ala  
           130                                  135                                  140

Gln Asn Lys Glu Gln Gln Val Lys Phe Gln Glu Gln Ile Lys Lys Ile  
 145                                  150                                  155                                  160

Glu Asp Asn Ile Ala Glu Ser Lys Lys Ser Gly Ile Leu Lys Phe Phe  
                   165                                  170                                  175

Gln Lys Leu Phe Ala Val Ile Gly Ala Val Leu Gly Ala Ile Gly Gly  
                   180                                  185                                  190

Ala Leu Ala Ile Ala Ala Gly Ala Ala Ser Gly Asn Pro Leu Leu Val  
           195                                  200                                  205

Ala Ala Gly Ile Met Ala Ile Val Ala Ser Ile Asp Ala Ala Met Ser  
           210                                  215                                  220

Ser Leu Ser Asp Gly Lys Val Ser Ile Ser Ala Gly Ile Ser Lys Ala  
 225                                  230                                  235                                  240

Leu Glu Ala Met Gly Val Pro Ala Glu Thr Ala Gln Trp Ile Ala Phe  
                   245                                  250                                  255

Gly Ile Gln Leu Ala Met Ile Ala Val Thr Ile Ala Ile Gly Phe Ala  
                   260                                  265                                  270

Ser Gly Gly Gly Gly Ala Met Ala Gly Val Ser Lys Ile Ala Asp Met  
 275 280 285

Phe Ser Lys Ser Gln Asp Val Ala Lys Leu Ala Gln Met Ile Glu Lys  
 290 295 300

Ala Ser Lys Ile Val Gln Ile Ala Gly Ser Val Asn Gln Ser Ala Ile  
 305 310 315 320

Gly Gly Thr Gly Ile Gly Thr Ala Val Val Gln Ser Asn Ile Lys Ala  
 325 330 335

Asn Glu Ser Glu Gln Lys Glu Ile Glu Ala Ala Ile Ala Lys Val Lys  
 340 345 350

Ala Lys Ile Glu Thr Leu Gln Asp Phe Phe Lys Asn Gln Met Glu Gln  
 355 360 365

Phe Asn Ala Ile Met Lys Ile Ile Thr Asp Ile Ile Gln Asp Ser Val  
 370 375 380

Asn Thr Lys Ile Ala Val Gln Arg Gly Ala Arg Glu  
 385 390 395

<210> 15  
 <211> 894  
 <212> DNA  
 <213> *Lawsonia intracellularis*

<220>  
 <221> CDS  
 <222> (13)..(894)

<400> 15  
 aggaggaatt at atg tct ctt gtc att aat aac aac ctg atg gcc gtc aat 51  
 Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn  
 1 5 10  
 gct caa cgt aac tta agc aag tct tat gga gaa ctg agt tct tct gtt 99  
 Ala Gln Arg Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val  
 15 20 25  
 cga aaa ctt tct tca ggt ctt cgt gta gga act gct gct gat gac tca 147  
 Arg Lys Leu Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser  
 30 35 40 45  
 gca ggg tta gcc att cga gaa ctc atg aga tct gac att gca aca aca 195  
 Ala Gly Leu Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr  
 50 55 60  
 caa caa gga ata cga aat gcg aat gat gct att tct atg att caa act 243  
 Gln Gln Gly Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr  
 65 70 75  
 gcg gat ggt gca ctt gga gtc atc gat gaa aag ctc att cga atg aaa 291

Ala Asp Gly Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys  
80 85 90

gaa ctt gct gaa caa gct gct aca ggt aca tat aac tcc act cag cgt 339  
Glu Leu Ala Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg  
95 100 105

atg att att gac tct gaa tat caa gct atg gcc tca gaa att act cgt 387  
Met Ile Ile Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg  
110 115 120 125

att gct aat gcg aca gaa ttt aat ggt ata aaa ctt ctt gat ggt tca 435  
Ile Ala Asn Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser  
130 135 140

tta tca ggt aat cat gat ggg aaa aaa ata aat tca act ggt gca gta 483  
Leu Ser Gly Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val  
145 150 155

cgt atc cac ttt ggg aca tct aac agc tct gct gaa gat tac tat gat 531  
Arg Ile His Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp  
160 165 170

att aaa att ggt ggc tct aca gct tct gca tta gga ctt ggt aat aca 579  
Ile Lys Ile Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr  
175 180 185

gta aaa ggt gcg ggt gct aca gtc tct act caa gct gca gca caa aat 627  
Val Lys Gly Ala Gly Thr Val Ser Thr Gln Ala Ala Ala Gln Asn  
190 195 200 205

gcc tta aaa gct ata gat aat gcc att gtt tca aaa gat aaa att cga 675  
Ala Leu Lys Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg  
210 215 220

gca cac ctt ggt gga tta caa aat aga ctt gaa gct aca gtt gat aat 723  
Ala His Leu Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn  
225 230 235

tta agt ata caa aat gaa aac tta caa gct gct gaa tct cgt ata tct 771  
Leu Ser Ile Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser  
240 245 250

gat ata gat gta agc caa gaa atg aca caa ttt gta cgt aac caa ata 819  
Asp Ile Asp Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile  
255 260 265

ctt aca caa aca ggt gtt gct atg ctt tca caa gct aat tct cta cca 867  
Leu Thr Gln Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro  
270 275 280 285

cgt atg gct cag caa ctt att ggc taa 894  
Arg Met Ala Gln Gln Leu Ile Gly  
290

<210> 16  
<211> 293  
<212> PRT  
<213> Lawsonia intracellularis

<400> 16

Met Ser Leu Val Ile Asn Asn Asn Leu Met Ala Val Asn Ala Gln Arg  
1 5 10 15

Asn Leu Ser Lys Ser Tyr Gly Glu Leu Ser Ser Ser Val Arg Lys Leu  
                   20                  25                  30

Ser Ser Gly Leu Arg Val Gly Thr Ala Ala Asp Asp Ser Ala Gly Leu  
           35                  40                  45

Ala Ile Arg Glu Leu Met Arg Ser Asp Ile Ala Thr Thr Gln Gln Gly  
       50                  55                  60

Ile Arg Asn Ala Asn Asp Ala Ile Ser Met Ile Gln Thr Ala Asp Gly  
   65                  70                  75                  80

Ala Leu Gly Val Ile Asp Glu Lys Leu Ile Arg Met Lys Glu Leu Ala  
                   85                  90                  95

Glu Gln Ala Ala Thr Gly Thr Tyr Asn Ser Thr Gln Arg Met Ile Ile  
                   100                  105                  110

Asp Ser Glu Tyr Gln Ala Met Ala Ser Glu Ile Thr Arg Ile Ala Asn  
       115                  120                  125

Ala Thr Glu Phe Asn Gly Ile Lys Leu Leu Asp Gly Ser Leu Ser Gly  
       130                  135                  140

Asn His Asp Gly Lys Lys Ile Asn Ser Thr Gly Ala Val Arg Ile His  
   145                  150                  155                  160

Phe Gly Thr Ser Asn Ser Ser Ala Glu Asp Tyr Tyr Asp Ile Lys Ile  
                   165                  170                  175

Gly Gly Ser Thr Ala Ser Ala Leu Gly Leu Gly Asn Thr Val Lys Gly  
           180                  185                  190

Ala Gly Ala Thr Val Ser Thr Gln Ala Ala Ala Gln Asn Ala Leu Lys  
       195                  200                  205

Ala Ile Asp Asn Ala Ile Val Ser Lys Asp Lys Ile Arg Ala His Leu  
       210                  215                  220

Gly Gly Leu Gln Asn Arg Leu Glu Ala Thr Val Asp Asn Leu Ser Ile  
   225                  230                  235                  240

Gln Asn Glu Asn Leu Gln Ala Ala Glu Ser Arg Ile Ser Asp Ile Asp  
                   245                  250                  255

Val Ser Gln Glu Met Thr Gln Phe Val Arg Asn Gln Ile Leu Thr Gln  
           260                  265                  270



Thr Gly Val Ala Met Leu Ser Gln Ala Asn Ser Leu Pro Arg Met Ala  
 275 280 285

Gln Gln Leu Ile Gly  
 290

<210> 17  
 <211> 2848  
 <212> DNA  
 <213> Lawsonia intracellularis

<220>  
 <221> CDS  
 <222> (29) .. (2848)

<400> 17  
 accttaacta aaaaataaaa agaataatt atg tat aat ata att aat aag cat 52  
 Met Tyr Asn Ile Ile Asn Lys His  
 1 5

caa atc ata aaa att tta tta ttt tcc tta tgt gtt ttc ttt ttt aca 100  
 Gln Ile Ile Lys Ile Leu Leu Phe Ser Leu Cys Val Phe Phe Phe Thr  
 10 15 20

ctt aca gaa aaa caa aaa att tat gct gca gac gtc ttt ttt gag ggc 148  
 Leu Thr Glu Lys Gln Lys Ile Tyr Ala Ala Asp Val Phe Phe Glu Gly  
 25 30 35 40

aga acc gaa acc tta atc aat gta aac aaa cca ttt gat tct ttt ttt 196  
 Arg Thr Glu Thr Leu Ile Asn Val Asn Lys Pro Phe Asp Ser Phe Phe  
 45 50 55

gga ggt tct gac tct aca ata gga acc ctt gaa aca gga cct act aat 244  
 Gly Gly Ser Asp Ser Thr Ile Gly Thr Leu Glu Thr Gly Pro Thr Asn  
 60 65 70

ctt acc ttc aca aca gta gga gcc ttc cgc aat tct gtt ttc aga att 292  
 Leu Thr Phe Thr Thr Val Gly Ala Phe Arg Asn Ser Val Phe Arg Ile  
 75 80 85

att ggt ggt ggt agg tct agt ttt aac aac cca aat aca gtt aaa ggc 340  
 Ile Gly Gly Gly Arg Ser Ser Phe Asn Asn Pro Asn Thr Val Lys Gly  
 90 95 100

aat gtt act cta act gtt tat aat act gat gta gaa aga ata att ggt 388  
 Asn Val Thr Leu Thr Val Tyr Asn Thr Asp Val Glu Arg Ile Ile Gly  
 105 110 115 120

gca ggt atc agc aat aga gga ctt gta acc gtt act ggc tca gta aat 436  
 Ala Gly Ile Ser Asn Arg Gly Leu Val Thr Val Thr Gly Ser Val Asn  
 125 130 135

atg aag cta gaa aat gtt tct gtt act aga gga att tat ggt ggt gtc 484  
 Met Lys Leu Glu Asn Val Ser Val Thr Arg Gly Ile Tyr Gly Gly Val  
 140 145 150

tat act caa aat gga cat gta cta ggc tct atc aac atg cat ttg aaa 532  
 Tyr Thr Gln Asn Gly His Val Leu Gly Ser Ile Asn Met His Leu Lys  
 155 160 165

aac gtc caa act cca cta tta ata ggt tct gga gta agc aat gga cct 580

Asn Val Gln Thr Pro Leu Leu Ile Gly Ser Gly Val Ser Asn Gly Pro	
170 175 180	
aat cgt att act gta aat gga gac ata aac att gat gtt gaa gac tct	628
Asn Arg Ile Thr Val Asn Gly Asp Ile Asn Ile Asp Val Glu Asp Ser	
185 190 195 200	
agg att caa tat gta aac att aca gga gaa gta gat gca ggg ata aaa	676
Arg Ile Gln Tyr Val Asn Ile Thr Gly Glu Val Asp Ala Gly Ile Lys	
205 210 215	
gga aat gct act cta act gta aaa aaa tct act gtt gag ctt ata aac	724
Gly Asn Ala Thr Leu Thr Val Lys Lys Ser Thr Val Glu Leu Ile Asn	
220 225 230	
tct ggt aga ggt aat atc tta ggt aat ctc aaa ata tct ata gca gat	772
Ser Gly Arg Gly Asn Ile Leu Gly Asn Leu Lys Ile Ser Ile Ala Asp	
235 240 245	
tca aat ata agg ggg tta tca cca gta gac ttt ggt tct tca gta tat	820
Ser Asn Ile Arg Gly Leu Ser Pro Val Asp Phe Gly Ser Ser Val Tyr	
250 255 260	
ggg gac aca tct ata aat gta att aat tct cag att aat gat att act	868
Gly Asp Thr Ser Ile Asn Val Ile Asn Ser Gln Ile Asn Asp Ile Thr	
265 270 275 280	
ctt ata cca agg gct ggt gga atg ctt gta ggt cct gtt acc cta gat	916
Leu Ile Pro Arg Ala Gly Gly Met Leu Val Gly Pro Val Thr Leu Asp	
285 290 295	
atc aca agc agt act ata caa aat ata caa tgt ggg cct gtc agt caa	964
Ile Thr Ser Ser Thr Ile Gln Asn Ile Gln Cys Gly Pro Val Ser Gln	
300 305 310	
aat aat caa ctt aac aca cta aat gta act gtt aat act agt aac att	1012
Asn Asn Gln Leu Asn Thr Leu Asn Val Thr Val Asn Thr Ser Asn Ile	
315 320 325	
act aac tta aac ctt ggt agt gtc gaa ggt cat aca ata tca act aca	1060
Thr Asn Leu Asn Leu Gly Ser Val Glu Gly His Thr Ile Ser Thr Thr	
330 335 340	
gca act gtt act gat agt aat att act aac ctt aat gtc gga acc ttc	1108
Ala Thr Val Thr Asp Ser Asn Ile Thr Asn Leu Asn Val Gly Thr Phe	
345 350 355 360	
aat gga ctt gga gta act gag aat gcc tct gta atc att aat agt ggc	1156
Asn Gly Leu Gly Val Thr Glu Asn Ala Ser Val Ile Ile Asn Ser Gly	
365 370 375	
aat att act aac ctt aat gtc gga act aat gta ata gct gca gcc aca	1204
Asn Ile Thr Asn Leu Asn Val Gly Thr Asn Val Ile Ala Ala Ala Thr	
380 385 390	
act att aat tcc tct gcg acc ata cac gac gga ctt att gca aac ctt	1252
Thr Ile Asn Ser Ser Ala Thr Ile His Asp Gly Leu Ile Ala Asn Leu	
395 400 405	
acc tta ggc tca caa ggt aat ggt cgt act atg ata gct aca gca aat	1300
Thr Leu Gly Ser Gln Gly Asn Gly Arg Thr Met Ile Ala Thr Ala Asn	
410 415 420	
gtt aat ggt gga act att gga tta tta act atg ggt tca gaa aac ttc	1348
Val Asn Gly Gly Thr Ile Gly Leu Leu Thr Met Gly Ser Glu Asn Phe	

425	430	435	440	
ata cca ggc aca aga cca att act gaa tta gca ata cta aac atg tct				1396
Ile Pro Gly Thr Arg Pro Ile Thr Glu Leu Ala Ile Leu Asn Met Ser				
	445	450	455	
ggg gga tta att gaa aga att atc gta ggt aat gcc aac tct tca acc				1444
Gly Gly Leu Ile Glu Arg Ile Ile Val Gly Asn Ala Asn Ser Ser Thr				
	460	465	470	
ata aac ttt act cct ggg aag aga tca att gta aaa aca ata aat ggt				1492
Ile Asn Phe Thr Pro Gly Lys Arg Ser Ile Val Lys Thr Ile Asn Gly				
	475	480	485	
cca gaa ctt cca tat tta gtt aac ata caa aaa ggt gct atg aca caa				1540
Pro Glu Leu Pro Tyr Leu Val Asn Ile Gln Lys Gly Ala Met Thr Gln				
	490	495	500	
tgg ggc act aaa aat atg ccc ttt tta ttg gat aca aga aat tta atc				1588
Trp Gly Thr Lys Asn Met Pro Phe Leu Leu Asp Thr Arg Asn Leu Ile				
	505	510	515	520
ttg tcc gga act ctg att acc tca aat att caa cta gct gat tta tct				1636
Leu Ser Gly Thr Leu Ile Thr Ser Asn Ile Gln Leu Ala Asp Leu Ser				
	525	530	535	
ata acc aat cta ttt gtt gct aat ggc ggt aca cta gta cct aga aaa				1684
Ile Thr Asn Leu Phe Val Ala Asn Gly Gly Thr Leu Val Pro Arg Lys				
	540	545	550	
tta ata cct ggg aac caa cct gtt ata cag ttt ctt gga ggt cct caa				1732
Leu Ile Pro Gly Asn Gln Pro Val Ile Gln Phe Leu Gly Gly Pro Gln				
	555	560	565	
tca ctc tta gtt atc cat caa cca tta aaa gta aat tta agc tta tca				1780
Ser Leu Leu Val Ile His Gln Pro Leu Lys Val Asn Leu Ser Leu Ser				
	570	575	580	
cca aaa ctt att gga agt agc atg gtg cca ctt gct ttt gtc tct caa				1828
Pro Lys Leu Ile Gly Ser Ser Met Val Pro Leu Ala Phe Val Ser Gln				
	585	590	595	600
tct ttt tca tca cca gat ctt ttt gtt aaa caa act aga agt ggt ctc				1876
Ser Phe Ser Ser Pro Asp Leu Phe Val Lys Gln Thr Arg Ser Gly Leu				
	605	610	615	
att tgg agt gat ctt gag ttt gat cca aca aca tct att tgg tat gtt				1924
Ile Trp Ser Asp Leu Glu Phe Asp Pro Thr Thr Ser Ile Trp Tyr Val				
	620	625	630	
aat aat atc caa gca tct caa gat ttt tac tct ttc tct att gct cgt				1972
Asn Asn Ile Gln Ala Ser Gln Asp Phe Tyr Ser Phe Ser Ile Ala Arg				
	635	640	645	
gag act act aac tgg cta aga caa caa cat ata tgg act cta caa aac				2020
Glu Thr Thr Asn Trp Leu Arg Gln Gln His Ile Trp Thr Leu Gln Asn				
	650	655	660	
cgt tca agt aaa ctt tta gac aac gaa cat tat gga cta tgg ata aat				2068
Arg Ser Ser Lys Leu Leu Asp Asn Glu His Tyr Gly Leu Trp Ile Asn				
	665	670	675	680
gtt caa ggt gga cat gaa agt ctt gat act tct att ggt agc aaa gca				2116
Val Gln Gly Gly His Glu Ser Leu Asp Thr Ser Ile Gly Ser Lys Ala				
	685	690	695	

aaa atg cca tgg ata atg gca aca gca gga tat gac tat ctt caa caa Lys Met Pro Trp Ile Met Ala Thr Ala Gly Tyr Asp Tyr Leu Gln Gln 700 705 710	2164
cta cca agg tta gat atg aaa gcc ctt tat ggt ctt gct ttt ggt gct Leu Pro Arg Leu Asp Met Lys Ala Leu Tyr Gly Leu Ala Phe Gly Ala 715 720 725	2212
tct aaa ggt aaa agt aaa tgg tct agc gtc aac tct aca aaa aat gat Ser Lys Gly Lys Ser Lys Trp Ser Ser Val Asn Ser Thr Lys Asn Asp 730 735 740	2260
gct gag cta ggt atg gtt agt ggt tat gta ggt ctt atc cat aac aaa Ala Glu Leu Gly Met Val Ser Gly Tyr Val Gly Leu Ile His Asn Lys 745 750 755 760	2308
act ggg ctc tat agt aca ttg acc tta caa ctt gcg tct agt aaa tta Thr Gly Leu Tyr Ser Thr Leu Thr Leu Gln Leu Ala Ser Ser Lys Leu 765 770 775	2356
cat act aat tct aca ggg ttc tat aga aat ttt aaa tgg aca gaa aca His Thr Asn Ser Thr Gly Phe Tyr Arg Asn Phe Lys Trp Thr Glu Thr 780 785 790	2404
act cca aca gaa gca ctt gaa ctt gga tgg aaa tac act ttc aac aac Thr Pro Thr Glu Ala Leu Glu Leu Gly Trp Lys Tyr Thr Phe Asn Asn 795 800 805	2452
ggt att aaa atg aat cct cgt gga caa ctt att ttt gaa caa aca tct Gly Ile Lys Met Asn Pro Arg Gly Gln Leu Ile Phe Glu Gln Thr Ser 810 815 820	2500
aaa cac cat ttt gat tta gga att caa aat gat aag gct ata tta gat Lys His His Phe Asp Leu Gly Ile Gln Asn Asp Lys Ala Ile Leu Asp 825 830 835 840	2548
aaa agc cag tta ata aca agt tct ctt ggt att acc gtt gaa tat aag Lys Ser Gln Leu Ile Thr Ser Ser Leu Gly Ile Thr Val Glu Tyr Lys 845 850 855	2596
cta cca gtt acc aca cct att aat ctt tat gct ggt att gaa agg ata Leu Pro Val Thr Thr Pro Ile Asn Leu Tyr Ala Gly Ile Glu Arg Ile 860 865 870	2644
aaa ggt cag tct gga aac ttt gca att agt tcc cag agc ctt caa atg Lys Gly Gln Ser Gly Asn Phe Ala Ile Ser Ser Gln Ser Leu Gln Met 875 880 885	2692
aag ttc aag cat gac aat gat aca agt gta gtt aga gca aca ata ggt Lys Phe Lys His Asp Asn Asp Thr Ser Val Val Arg Ala Thr Ile Gly 890 895 900	2740
aca aat ata tta ttg gga gaa cat ttt aat att cac tgt gat ata ttt Thr Asn Ile Leu Leu Gly Glu His Phe Asn Ile His Cys Asp Ile Phe 905 910 915 920	2788
gga gat aaa gga aat gat aaa ggc att ggt ggg caa gca gga ttt aca Gly Asp Lys Gly Asn Asp Lys Gly Ile Gly Gly Gln Ala Gly Phe Thr 925 930 935	2836
tac aaa ttt taa Tyr Lys Phe	2848

<210> 18  
 <211> 939  
 <212> PRT  
 <213> *Lawsonia intracellularis*  
 <400> 18  
 Met Tyr Asn Ile Ile Asn Lys His Gln Ile Ile Lys Ile Leu Leu Phe  
 1 5 10 15  
 Ser Leu Cys Val Phe Phe Phe Thr Leu Thr Glu Lys Gln Lys Ile Tyr  
 20 25 30  
 Ala Ala Asp Val Phe Phe Glu Gly Arg Thr Glu Thr Leu Ile Asn Val  
 35 40 45  
 Asn Lys Pro Phe Asp Ser Phe Phe Gly Gly Ser Asp Ser Thr Ile Gly  
 50 55 60  
 Thr Leu Glu Thr Gly Pro Thr Asn Leu Thr Phe Thr Thr Val Gly Ala  
 65 70 75 80  
 Phe Arg Asn Ser Val Phe Arg Ile Ile Gly Gly Gly Arg Ser Ser Phe  
 85 90 95  
 Asn Asn Pro Asn Thr Val Lys Gly Asn Val Thr Leu Thr Val Tyr Asn  
 100 105 110  
 Thr Asp Val Glu Arg Ile Ile Gly Ala Gly Ile Ser Asn Arg Gly Leu  
 115 120 125  
 Val Thr Val Thr Gly Ser Val Asn Met Lys Leu Glu Asn Val Ser Val  
 130 135 140  
 Thr Arg Gly Ile Tyr Gly Gly Val Tyr Thr Gln Asn Gly His Val Leu  
 145 150 155 160  
 Gly Ser Ile Asn Met His Leu Lys Asn Val Gln Thr Pro Leu Leu Ile  
 165 170 175  
 Gly Ser Gly Val Ser Asn Gly Pro Asn Arg Ile Thr Val Asn Gly Asp  
 180 185 190  
 Ile Asn Ile Asp Val Glu Asp Ser Arg Ile Gln Tyr Val Asn Ile Thr  
 195 200 205  
 Gly Glu Val Asp Ala Gly Ile Lys Gly Asn Ala Thr Leu Thr Val Lys  
 210 215 220  
 Lys Ser Thr Val Glu Leu Ile Asn Ser Gly Arg Gly Asn Ile Leu Gly

225		230		235		240									
Asn	Leu	Lys	Ile	Ser	Ile	Ala	Asp	Ser	Asn	Ile	Arg	Gly	Leu	Ser	Pro
				245					250					255	
Val	Asp	Phe	Gly	Ser	Ser	Val	Tyr	Gly	Asp	Thr	Ser	Ile	Asn	Val	Ile
			260					265					270		
Asn	Ser	Gln	Ile	Asn	Asp	Ile	Thr	Leu	Ile	Pro	Arg	Ala	Gly	Gly	Met
		275					280					285			
Leu	Val	Gly	Pro	Val	Thr	Leu	Asp	Ile	Thr	Ser	Ser	Thr	Ile	Gln	Asn
	290					295					300				
Ile	Gln	Cys	Gly	Pro	Val	Ser	Gln	Asn	Asn	Gln	Leu	Asn	Thr	Leu	Asn
305					310					315					320
Val	Thr	Val	Asn	Thr	Ser	Asn	Ile	Thr	Asn	Leu	Asn	Leu	Gly	Ser	Val
			325						330					335	
Glu	Gly	His	Thr	Ile	Ser	Thr	Thr	Ala	Thr	Val	Thr	Asp	Ser	Asn	Ile
			340					345					350		
Thr	Asn	Leu	Asn	Val	Gly	Thr	Phe	Asn	Gly	Leu	Gly	Val	Thr	Glu	Asn
	355						360					365			
Ala	Ser	Val	Ile	Ile	Asn	Ser	Gly	Asn	Ile	Thr	Asn	Leu	Asn	Val	Gly
	370					375					380				
Thr	Asn	Val	Ile	Ala	Ala	Ala	Thr	Thr	Ile	Asn	Ser	Ser	Ala	Thr	Ile
385				390						395					400
His	Asp	Gly	Leu	Ile	Ala	Asn	Leu	Thr	Leu	Gly	Ser	Gln	Gly	Asn	Gly
			405						410					415	
Arg	Thr	Met	Ile	Ala	Thr	Ala	Asn	Val	Asn	Gly	Gly	Thr	Ile	Gly	Leu
			420					425					430		
Leu	Thr	Met	Gly	Ser	Glu	Asn	Phe	Ile	Pro	Gly	Thr	Arg	Pro	Ile	Thr
	435						440					445			
Glu	Leu	Ala	Ile	Leu	Asn	Met	Ser	Gly	Gly	Leu	Ile	Glu	Arg	Ile	Ile
	450					455					460				
Val	Gly	Asn	Ala	Asn	Ser	Ser	Thr	Ile	Asn	Phe	Thr	Pro	Gly	Lys	Arg
465				470						475					480
Ser	Ile	Val	Lys	Thr	Ile	Asn	Gly	Pro	Glu	Leu	Pro	Tyr	Leu	Val	Asn
			485						490					495	

Ile Gln Lys Gly Ala Met Thr Gln Trp Gly Thr Lys Asn Met Pro Phe  
 500 505 510

Leu Leu Asp Thr Arg Asn Leu Ile Leu Ser Gly Thr Leu Ile Thr Ser  
 515 520 525

Asn Ile Gln Leu Ala Asp Leu Ser Ile Thr Asn Leu Phe Val Ala Asn  
 530 535 540

Gly Gly Thr Leu Val Pro Arg Lys Leu Ile Pro Gly Asn Gln Pro Val  
 545 550 555 560

Ile Gln Phe Leu Gly Gly Pro Gln Ser Leu Leu Val Ile His Gln Pro  
 565 570 575

Leu Lys Val Asn Leu Ser Leu Ser Pro Lys Leu Ile Gly Ser Ser Met  
 580 585 590

Val Pro Leu Ala Phe Val Ser Gln Ser Phe Ser Ser Pro Asp Leu Phe  
 595 600 605

Val Lys Gln Thr Arg Ser Gly Leu Ile Trp Ser Asp Leu Glu Phe Asp  
 610 615 620

Pro Thr Thr Ser Ile Trp Tyr Val Asn Asn Ile Gln Ala Ser Gln Asp  
 625 630 635 640

Phe Tyr Ser Phe Ser Ile Ala Arg Glu Thr Thr Asn Trp Leu Arg Gln  
 645 650 655

Gln His Ile Trp Thr Leu Gln Asn Arg Ser Ser Lys Leu Leu Asp Asn  
 660 665 670

Glu His Tyr Gly Leu Trp Ile Asn Val Gln Gly Gly His Glu Ser Leu  
 675 680 685

Asp Thr Ser Ile Gly Ser Lys Ala Lys Met Pro Trp Ile Met Ala Thr  
 690 695 700

Ala Gly Tyr Asp Tyr Leu Gln Gln Leu Pro Arg Leu Asp Met Lys Ala  
 705 710 715 720

Leu Tyr Gly Leu Ala Phe Gly Ala Ser Lys Gly Lys Ser Lys Trp Ser  
 725 730 735

Ser Val Asn Ser Thr Lys Asn Asp Ala Glu Leu Gly Met Val Ser Gly  
 740 745 750

Tyr Val Gly Leu Ile His Asn Lys Thr Gly Leu Tyr Ser Thr Leu Thr  
 755 760 765

Leu Gln Leu Ala Ser Ser Lys Leu His Thr Asn Ser Thr Gly Phe Tyr  
 770 775 780

Arg Asn Phe Lys Trp Thr Glu Thr Thr Pro Thr Glu Ala Leu Glu Leu  
 785 790 795 800

Gly Trp Lys Tyr Thr Phe Asn Asn Gly Ile Lys Met Asn Pro Arg Gly  
 805 810 815

Gln Leu Ile Phe Glu Gln Thr Ser Lys His His Phe Asp Leu Gly Ile  
 820 825 830

Gln Asn Asp Lys Ala Ile Leu Asp Lys Ser Gln Leu Ile Thr Ser Ser  
 835 840 845

Leu Gly Ile Thr Val Glu Tyr Lys Leu Pro Val Thr Thr Pro Ile Asn  
 850 855 860

Leu Tyr Ala Gly Ile Glu Arg Ile Lys Gly Gln Ser Gly Asn Phe Ala  
 865 870 875 880

Ile Ser Ser Gln Ser Leu Gln Met Lys Phe Lys His Asp Asn Asp Thr  
 885 890 895

Ser Val Val Arg Ala Thr Ile Gly Thr Asn Ile Leu Leu Gly Glu His  
 900 905 910

Phe Asn Ile His Cys Asp Ile Phe Gly Asp Lys Gly Asn Asp Lys Gly  
 915 920 925

Ile Gly Gly Gln Ala Gly Phe Thr Tyr Lys Phe  
 930 935